

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2005, 18:02:30 ; Search time 105.833 Seconds
(without alignments)
54.366 Million cell updates/sec

Title: US-10-083-768-5
Perfect score: 25
Sequence: 1 XXGXXXXXXW 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	68.0	72	Q98PI6	Q98pi6 mycoplasma
2	17	68.0	83	Q726B3	Q726b3 desulfovibrio
3	17	68.0	83	AA597722	AA597722 desulfovi
4	17	68.0	87	Q7SA05	Q7sad5 neurospora
5	17	68.0	98	Q8RNZ2	Q8rnz2 pseudomonas
6	17	68.0	102	Q6H418	Q6h418 oryza sativ
7	17	68.0	109	Q72KT8	Q72kt8 thermus t
8	17	68.0	109	AA580777	AA580777 thermus t
9	17	68.0	127	Q5ZF42	Q5zf42 oryza sativ
10	17	68.0	127	BAC83391	Bac83391 oryza sat
11	17	68.0	132	1 YBL2_STRCI	P33654 streptomyce
12	17	68.0	133	Q6Z0D1	Q6z0d1 oryza sativ
13	17	68.0	133	BAD03254	Bad03254 oryza sat
14	17	68.0	133	BAD03677	Bad03677 oryza sat
15	17	68.0	137	Q36EH8	Q36eh8 homo sapien
16	17	68.0	143	Q855T6	Q855t6 mycobacteri
17	17	68.0	148	Q870Y5	Q870y5 neurospora
18	17	68.0	150	Q7XP55	Q7xp55 oryza sativ
19	17	68.0	151	Q9K3P1	Q9k3p1 streptomyce
20	17	68.0	156	Q3FN29	Q3fn29 arabidopsis
21	17	68.0	165	Q311B2	Q311b2 pseudomonas
22	17	68.0	175	Q983U3	Q983u3 rhizobium l
23	17	68.0	181	Q9QU0D	Q9qu0d tt virus. o
24	17	68.0	181	Q9QU0D1	Q9qu0d1 tt virus. o
25	17	68.0	181	Q9QU0D2	Q9qu0d2 tt virus. o
26	17	68.0	181	Q9QU0D3	Q9qu0d3 tt virus. o
27	17	68.0	190	Q8FG89	Q8fg89 xanthomonas
28	17	68.0	192	Q82G39	Q82g39 streptomyce
29	17	68.0	196	Q7PCT4	Q7pct4 anopheles g
30	17	68.0	196	Q8PP95	Q8pp95 xanthomonas
31	17	68.0	203	1 SODM_HALWA	Q03302 haloarcula

32 17 68.0 211 2 Q87X57 Q87x57 pseudomonas
33 17 68.0 211 2 Q8U219 Q8u219 phocoena sp
34 17 68.0 212 2 Q61CK5 Q61ck5 homo sapien
35 17 68.0 212 2 CAG30249 Cag30249 homo sapi
36 17 68.0 220 2 Q9WKT8 Q9wkt8 tt virus. h
37 17 68.0 221 2 Q872B6 Q872b6 neurospora
38 17 68.0 224 2 Q9DT84 Q9dt84 tt virus. o
39 17 68.0 224 2 Q9DT85 Q9dt85 tt virus. o
40 17 68.0 224 2 Q9DT86 Q9dt86 tt virus. o
41 17 68.0 224 2 Q9DT87 Q9dt87 tt virus. o
42 17 68.0 224 2 Q9DT88 Q9dt88 tt virus. o
43 17 68.0 224 2 Q9DT89 Q9dt89 tt virus. o
44 17 68.0 224 2 Q9DT90 Q9dt90 tt virus. o
45 17 68.0 224 2 Q9DT91 Q9dt91 tt virus. o

ALIGNMENTS

RESULT 1

Q98PI6 ID Q98PI6 PRELIMINARY; PRT; 72 AA.
AC Q98PI6;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein MYPU_7360.
GN OrderedLocusNames=MYPU_7360;
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RX MEDLINE=21267165; PubMed=11353084;
RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis.";
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL; AL445565; CAC13909.1; -
DR PIR; H90603; H90603.
DR MYPUList; MYPU_7360; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 72 AA; 7389 MW; F8D944A953945DF4 CRC64;
Query Match 68.0%; Score 17; DB 2; Length 72;
Best Local Similarity 28.6%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 39 GAAATSW 45

RESULT 2

Q726B3 ID Q726B3 PRELIMINARY; PRT; 83 AA.
AC Q726B3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=DVU3252;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15077118; DOI=10.1038/nbt959;

```

RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RA "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough.";
RL Nat. Biotechnol. 22:554-559 (2004).
DR EMBL; AF017320; AAS97722.1; -.
DR TIGR; DVU3252; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 83 AA; 9109 MW; 463F6FFADD2D0D05 CRC64;

Query Match 68.0%; Score 17; DB 2; Length 83;
Best Local Similarity 28.6%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 57 GSTTAAW 63

RESULT 3
AAS97722 PRELIMINARY; PRT; 83 AA.
AC AAS97722;
DT 26-APR-2004 (TrEMBLrel. 27, Created)
DT 26-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN DVU3252.
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15077118;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RA "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough.";
RL Nat. Biotechnol. 22:554-559 (2004).
DR EMBL; AF017320; AAS97722.1; -.
DR TIGR; DVU3252; -.
KW Hypothetical protein.
SQ SEQUENCE 83 AA; 9109 MW; 463F6FFADD2D0D05 CRC64;

Query Match 68.0%; Score 17; DB 2; Length 83;
Best Local Similarity 28.6%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 57 GSTTAAW 63

RESULT 4
Q7SAD5 PRELIMINARY; PRT; 87 AA.
AC Q7SAD5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.

```

```

GN Name=NCU06295.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Renman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysellis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Eboile D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0 (2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000205; EAA33321.1; -.
SQ SEQUENCE 87 AA; 8712 MW; 19B486AC40439088 CRC64;

Query Match 68.0%; Score 17; DB 2; Length 87;
Best Local Similarity 28.6%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 30 GTSSSAW 36

RESULT 5
Q8RN22 PRELIMINARY; PRT; 98 AA.
AC Q8RN22;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative type III effector Holptov (fragment).
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=21862332; PubMed=11872842;
RA Guttman D.S., Vinatzer B.A., Sarkar S.F., Ranall M.V., Kettler G.,
RA Greenberg J.T.;
RT "A Functional Screen for the Type III (Hrp) Secretome of the Plant
Pathogen Pseudomonas syringae.";
RL Science 295:1722-1726 (2002).
DR EMBL; AF458401; AAL84265.1; -.
FT NON TER 98
SQ SEQUENCE 98 AA; 11011 MW; A85EFB004F40D45 CRC64;

Query Match 68.0%; Score 17; DB 2; Length 98;
Best Local Similarity 28.6%; Pred. No. 7.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXX 9
Db 6 GSSSATW 12

```

RESULT 6

Q6H418 PRELIMINARY; PRT; 102 AA.
 ID Q6H418;
 AC Q6H418;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein P0599F09.8.
 GN Name=P0599F09.8;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriatoidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005867; BAD26361.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 102 AA; 10257 MW; 2330B2E1FB71DDEC CRC64;

Query Match 68.0%; Score 17; DB 2; Length 102;
 Best Local Similarity 28.6%; Pred. No. 7.8e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXW 9
 Db 70 GAAAAW 76

RESULT 7

Q72KT8 PRELIMINARY; PRT; 109 AA.
 ID Q72KT8;
 AC Q72KT8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical membrane spanning protein.
 GN OrderedLocusNames=TPC0429;
 OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=262724;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Henne A., Brueggemann H., Raasch C., Wierzer A., Hartsch T.,
 RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
 RA Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
 RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
 RT "The genome sequence of the extreme thermophile Thermus
 thermophilus".
 RL Nat. Biotechnol. 22:547-553 (2004).
 DR EMBL; AE017302; AAS80777.1; -;
 DR InterPro; IPR005530; SPW.
 DR Pfam; PF03779; SPW; 2.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 109 AA; 11814 MW; BL43CD19CA62593P CRC64;

Query Match 68.0%; Score 17; DB 2; Length 109;
 Best Local Similarity 28.6%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXW 9
 Db 27 GTSSATW 33

RESULT 8

AAS80777 PRELIMINARY; PRT; 109 AA.
 ID AAS80777
 AC AAS80777;

DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DS Hypothetical membrane spanning protein.
 GN TFC0429.
 OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=262724;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Henne A., Brueggemann H., Raasch C., Wierzer A., Hartsch T.,
 RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
 RA Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
 RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
 RT "The genome sequence of the extreme thermophile Thermus
 thermophilus".
 RL Nat. Biotechnol. 22:547-553 (2004).
 DR EMBL; AE017302; AAS80777.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 109 AA; 11814 MW; BL43CD19CA62593P CRC64;

Query Match 68.0%; Score 17; DB 2; Length 109;
 Best Local Similarity 28.6%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXW 9
 Db 27 GTSSATW 33

RESULT 9

Q6ZF42 PRELIMINARY; PRT; 127 AA.
 ID Q6ZF42;
 AC Q6ZF42;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein P0406F06.31.
 GN Name=P0406F06.31;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriatoidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004370; BAC83391.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 127 AA; 13838 MW; 6F74D278AC08AF0C CRC64;

Query Match 68.0%; Score 17; DB 2; Length 127;
 Best Local Similarity 28.6%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXXW 9
 Db 24 GTSSATW 30

RESULT 10

BAC83391 PRELIMINARY; PRT; 127 AA.
 ID BAC83391
 AC BAC83391;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein P0406F06.31.
 GN P0406F06.31.
 OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.
 OK NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
 RT clone:PO406F06.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004270; BAC83391.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 127 AA; 13838 MW; 6F74D278AC08AF0C CRC64;
 Query Match 68.0%; Score 17; DB 2; Length 127;
 Best Local Similarity 28.6%; Pred. No. 9.4e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 GXXXXXXW 9
 DB 24 GTSTSAW 30
 RESULT 11
 YBL2_STRCI STANDARD; PRT; 132 AA.
 AC P33654;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypothetical 14.2 kDa protein in blaB 3' region.
 OS Streptomyces cacaoi.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OK NCBI_TaxID=1898;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KCC S0352;
 RX MEDLINE=92234939; PubMed=1569015;
 RA Urabe H., Ogawara H.;
 RT "Nucleotide sequence and transcriptional analysis of activator-
 RT regulator proteins for beta-lactamase in Streptomyces cacaoi.";
 RL J. Bacteriol. 174:2834-2842(1992).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D00937; BAA00776.1; -;
 DR FIR; C41855; C41855.
 KW Hypothetical protein.
 SQ SEQUENCE 132 AA; 14234 MW; FFD48A2182B52D8 CRC64;
 Query Match 68.0%; Score 17; DB 1; Length 132;
 Best Local Similarity 28.6%; Pred. No. 9.7e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 GXXXXXXW 9
 DB 53 GSSASSW 59
 RESULT 12
 Q620D1 PRELIMINARY; PRT; 133 AA.
 ID Q620D1
 AC Q620D1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein OSJNBa0078D03.43 (Hypothetical protein
 DE P0703C03.23).
 GN Name=OSJNBa0078D03.43; Synonyms=P0703C03.23;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OK NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005493; BAD03677.1; -;
 DR EMBL; AP004637; BAD03254.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 133 AA; 14574 MW; 9F18BC7F0A45B2BA CRC64;
 Query Match 68.0%; Score 17; DB 2; Length 133;
 Best Local Similarity 28.6%; Pred. No. 9.8e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 GXXXXXXW 9
 DB 38 GTAAAW 44
 RESULT 13
 BAD03254 PRELIMINARY; PRT; 133 AA.
 ID BAD03254;
 AC BAD03254;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein P0703C03.23.
 GN P0703C03.23.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.
 OK NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, PAC
 RT clone:P0703C03.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004637; BAD03254.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 133 AA; 14574 MW; 9F18BC7F0A45B2BA CRC64;
 Query Match 68.0%; Score 17; DB 2; Length 133;
 Best Local Similarity 28.6%; Pred. No. 9.8e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 GXXXXXXW 9
 DB 38 GTAAAW 44
 RESULT 14
 BAD03677 PRELIMINARY; PRT; 133 AA.
 ID BAD03677;
 AC BAD03677;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein OSJNBa0078D03.43.

GN OSJNBA0078D03.43.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC
 clone OSJNBA0078D03.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005493; BAD03677.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 133 AA; 14574 MW; 9F18BC7F0A45B2A CRC64;

Query Match 68.0%; Score 17; DB 2; Length 133;
 Best Local Similarity 28.6%; Pred. No. 9.8e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GXXXXXW 9
 DB 38 GTAAAW 44

RESULT 15
 Q96EH8
 ID Q96EH8 PRELIMINARY; PRT; 137 AA.
 AC Q96EH8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein LOC93082.
 GN Name=LOC93082;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC012317; AAH12317.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 137 AA; 14308 MW; 53A2EF0CB2BCFB78 CRC64;

Query Match 68.0%; Score 17; DB 2; Length 137;

Best Local Similarity 28.6%; Pred. No. 1e+04;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 GXXXXXW 9
 DB 52 GAAASAW 58

Search completed: January 31, 2005, 18:21:40
 Job time : 107.833 secs

THIS PAGE LEFT BLANK